

FIGURE 1

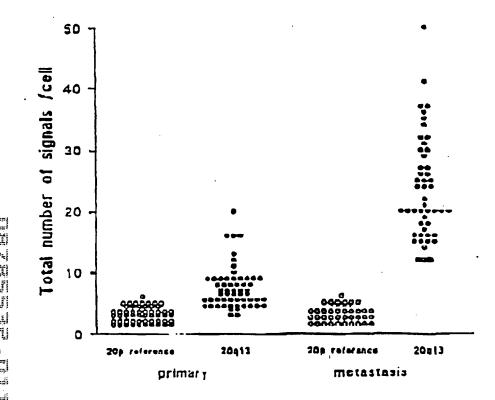


FIGURE 2

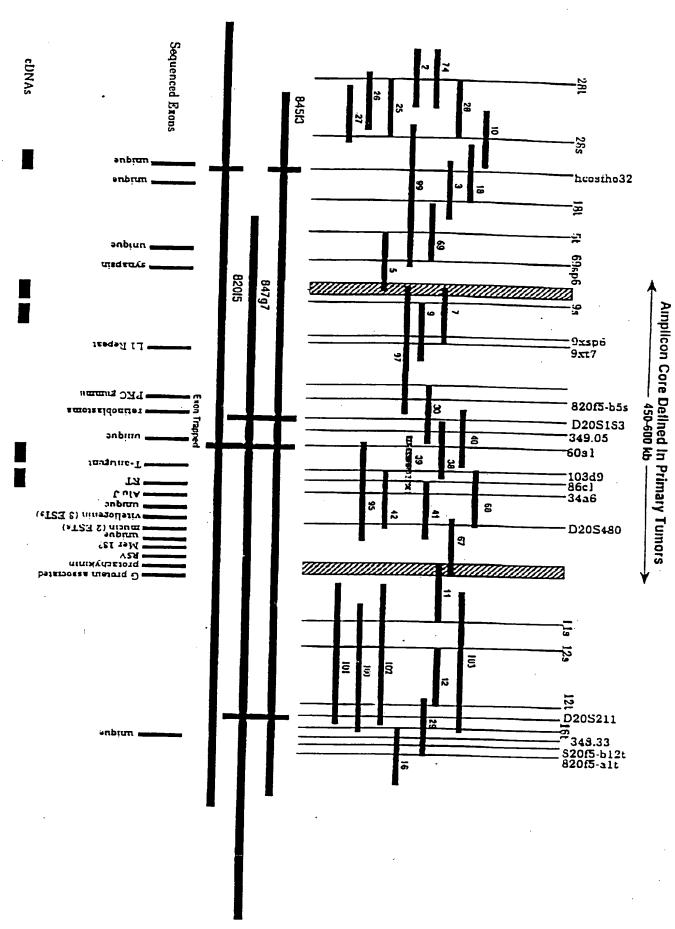


FIGURE 3

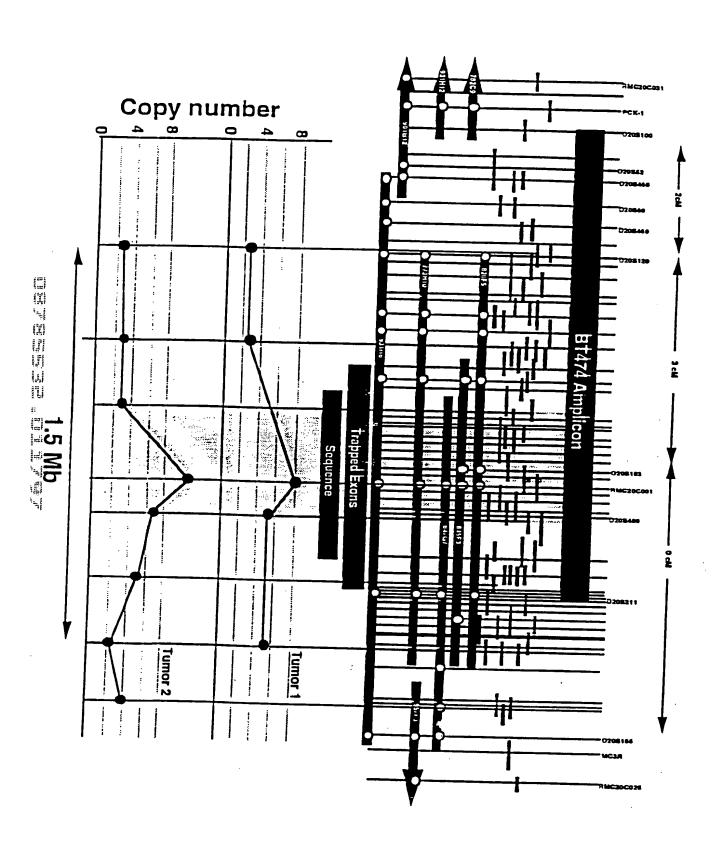


FIGURE 4

The state of the s

ene ID

6, 7, 8, 9, 10, 11

12, 13, 14, 15

Genomic Sequence from BAC clone 97 -Filtered query sequence >query\_seq

**ECACCTTGCCAAACATCACACGC'PTG** TGTGATATTGATTCATGCCCT CCATCCAGTCCACTCGATTTTGGCAGTGCAGATGAAAAACTGGGAACCAT TTGTGTTGAGTCCAGCAAGATGCCAGGACCTGCATGTTTCAGAACGAAGT TCTTCATCATCCAATTTCTCCCTGTATATGGGCTTACCACNACTGCCGTT AAGTCGTGTNAAGTCACCACTCAGGTACATAATGGAATAATTCTGCAAAG GCAGGAGNCACTTTCTCTCCAGTGCTCAGACCATGAAAGTTTTCTGATGT CTTTGGAACTTTGTCTGCAAATAGCTCGAAGGAGACATGGCCTAAAGGCT CGCCATCTGCGGTGATATTGNAACATGGTAGGGCTGACCGTGGCTGTGGC NNNNNNNNNNNNNCCCAATGCGGGACAGAGAATCNAAGAAACTGTATTA GGGAAAGGGTCCTGAGTTTATGCCAAAGTTTCCCAGATTGCTTTCCATTG AAACGTAGCTCTGTGAGATACCATCAGGTGTTATGTGAAGAAATGTCTGT GCAAGACTTCCCATCTTCTGTCCCTTTTTATGCTAATGGGTAACACAAAC TCCAAAAGTGGGGTGTACAGCATGAGGCATTAACAAAAATTTATTGGACC 

gb|M19533|RATCYCA Rat cyclophilin mRNA, complete cds. Length = 743

Query:

Sbjct:

```
Minus Strand HSPs:
Score = 418 (115.5 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 96/112 (85%), Positives = 96/112 (85%), Strand = Minus /
Plus
       372 TNCAATATCACCGCAGATGGCGAGCCTTTAGGCCATGTCTCCTTCGAGCTATTTGCAGAC
Query:
313
           64 TTCGACATCACGCTGATGGCGAGCCCTTGGGTCGCGTCTGCTTCGAGCTGTTTGCAGAC
Sbjct:
123
       312 AAAGTTCCAAAGACATCAGAAAACTTTCATGGTCTGAGCACTGGAGAGAAAG 261
Query:
           124 AAAGTTCCAAAGACAGCAGAAAACTTTCGTGCTCTGAGCACTGGGGAGAAAG 175
Sbjct:
Score = 236 (65.2 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 52/58 (89%). Positives = 52/58 (89%). Strand = Minus / Plus
       117 TGCTGGACTCAACACAAATGGTTCCCAGTTTTTCATCTGCACTGCCAAAATCGAGTGG 60
Ouerv:
           Sbjct:
       348 TGCTGGACCAAACACAAATGGTTCCCAGTTTTTTATCTGCACTGCCAAGACTGAGTGG
405
Score = 177 (48.9 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 41/48 (85%). Positives = 41/48 (85%). Strand = Minus / Plus
        60 GACTGGATGGCAAGCGTGTGATGTTTGGCAAGGTGCAAGAGGGCATGA 13
Query:
           404 GGCTGGATGGCAAGCATGTGGTCTTTGGGAAGGTGAAAGAAGGCATGA 451
Sbjct:
Score = 154 (42.6 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 34/38 (89%), Positives = 34/38 (89%), Strand = Minus / Plus
       153 AGAACTTCGTTCTGAAACATGCAGGTCCTGGCATCTTG 116
Query:
           299 AGAACTTCATCCTGAAGCATACAGGTCCTGGCATCTTG 336
Sbict:
Score = 86 (23.8 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
```

Identities = 22/28 (79%), Positives = 22/28 (78%), Strand = Minus / Plus

Figure 6

256 TCCTGCCTTTGCAGAATTATTCCATTAT 229

193 TCCTCCTTTCACAGAATTATTCCAGGAT 220